

Structural Basis for Dimerization of Hepatitis Delta Antigen	X12C
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Data was collected on a peptide that corresponds to the oligomerization domain of hepatitis delta antigen. The hepatitis delta antigen is the only protein encoded by the Hepatitis D virus. This region of the protein (amino acids 12-60, which represent 25% of the full length protein) is important in replication of the virus. If dimerization does not take place the virus cannot replicate. The high intensity beam at X12C allowed us to collect a data set to 1.73E, which had a Rsym of 4.4% with an I/s of 45.1. This is a vast improvement over the quality of the data we have been able to collect in our own laboratory, a 2.2E dataset with Rsym of 5.9% with an I/s of 14.3.

We are still in the process of refining the structure to high resolution. With the aid of the high resolution data we have been able to model a number of sidechains with multiple conformers. We believe we can use the high resolution structure of the peptide to aid in the design of new antivirals for hepatitis D. The structure will also represent the first high resolution structure of an antiparallel coiled coil and may lend itself in the aid of designing new coiled coil structures.

The help from the staff at Brookhaven was indispensable. Not only were they sincerely interested in our input, but suggestions to programs were incorporated while we were there collecting our data. The X12C environment is extremely user friendly, from wet lab preparations to data collection to processing. Finally, I would like to emphasize that the data collection software at X12C is far superior to any other software I have used. I believe it made this the first actual pleasurable synchrotron trip I have ever been a part of.